



#4

1

## SEQUENCE LISTING

<110> Reiter, Yoram  
<120> SINGLE CHAIN CLASS I MAJOR HISTO-COMPATIBILITY COMPLEXES,  
CONSTRUCTS ENCODING SAME AND METHODS OF GENERATING SAME  
<130> 02/23338  
<150> US 10/075,257  
<151> 2002-02-15  
<160> 20  
<170> PatentIn version 3.2  
<210> 1  
<211> 9  
<212> PRT  
<213> Artificial sequence  
<220>  
<223> Cancer cell associated, synthetic peptide  
<400> 1

Ile Met Asp Gln Val Pro Phe Ser Val  
1 5

<210> 2  
<211> 9  
<212> PRT  
<213> Artificial sequence

<220>  
<223> Cancer cell associated, synthetic peptide  
<400> 2

Tyr Leu Glu Pro Gly Pro Val Thr Val  
1 5

<210> 3  
<211> 9  
<212> PRT  
<213> Artificial sequence

<220>  
<223> TAX 11-19 HTLV-1 control peptide  
<400> 3

Leu Leu Phe Gly Tyr Pro Val Tyr Val  
1 5

<210> 4  
<211> 1048  
<212> DNA  
<213> Homo sapiens

<400> 4  
atgatccagc gtactccaaa gattcaggtt tactcacgtc atccagcaga gaatggaaag 60  
tcaaatttcc tgaattgcta tgtgtctggg tttcatccat ccgacattga agttgactta 120  
ctgaagaatg gagagagaat tgaaaaagtg gagcattcag acttgtcttt cagcaaggac 180  
tggtctttct atctcttgta ttatactgag ttcaccccca ctgaaaaaga tgagtatgcc 240  
tgccgtgtga accacgtgac ttgtcacag cccaagatag ttaagtggga tcgagacatg 300

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ggtggcggtg gaagcggcgg tggaggctct ggtggaggtg gcagcggctc tcaactccatg 360
aggtatttct tcacatccgt gtcccggccc ggccgcgggg agccccgctt catcgcagtg 420
ggctacgtgg acgacacgca gttcgtgcgg ttcgacagcg acgccgcgag ccagaggatg 480
gagccgcggg cgccgtggat agagcaggag ggtccggagt attgggacgg ggagacacgg 540
aaagtgaagg cccactcaca gactcaccga gtggacctgg ggacctgcg cggctactac 600
aaccagagcg aggccggttc tcacaccgtc cagaggatgt atggctgcga cgtggggctcg 660
gactggcgct tcctccgcgg gtaccaccag tacgcctacg acggcaagga ttacatcgcc 720
ctgaaagagg acctgcgctc ttggaccgcg gcggacatgg cagctcagac caccaagcac 780
aagtgggagg cgcccatgt ggccggagcag ttgagagcct acctggaggg cacgtgcgtg 840
gagtggctcc gcagatacct ggagaacggg aaggagacgc tgcagcgcac ggacgcccc 900
aaaacgcaca tgactcacca cgctgtctct gaccatgaag ccaccctgag gtgctgggcc 960
ctgagcttct accctgcgga gatcacactg acctggcagc ggacttggag gaatctttga 1020
ggcaatgaag atggagctgc gggactga 1048

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<210> 5
<211> 415
<212> PRT
<213> Artificial sequence

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<220>
<223> Human beta2 microglobulin linked to MHC class I heavy chain
<400> 5

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Met Ile Gln Arg Thr Pro Lys Ile Gln Val Tyr Ser Arg His Pro Ala
1           5           10           15

```

```

Glu Asn Gly Lys Ser Asn Phe Leu Asn Cys Tyr Val Ser Gly Phe His
20           25           30

```

```

Pro Ser Asp Ile Glu Val Asp Leu Leu Lys Asn Gly Glu Arg Ile Glu
35           40           45

```

```

Lys Val Glu His Ser Asp Leu Ser Phe Ser Lys Asp Trp Ser Phe Tyr
50           55           60

```

```

Leu Leu Tyr Tyr Thr Glu Phe Thr Pro Thr Glu Lys Asp Glu Tyr Ala
65           70           75           80

```

```

Cys Arg Val Asn His Val Thr Leu Ser Gln Pro Lys Ile Val Lys Trp
85           90           95

```

```

Asp Arg Asp Met Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly
100          105          110

```

```

Gly Gly Ser Gly Ser His Ser Met Arg Tyr Phe Phe Thr Ser Val Ser
115          120          125

```

```

Arg Pro Gly Arg Gly Glu Pro Arg Phe Ile Ala Val Gly Tyr Val Asp
130          135          140

```

Asp Thr Gln Phe Val Arg Phe Asp Ser Asp Ala Ala Ser Gln Arg Met  
145 150 155 160

Glu Pro Arg Ala Pro Trp Ile Glu Gln Glu Gly Pro Glu Tyr Trp Asp  
165 170 175

Gly Glu Thr Arg Lys Val Lys Ala His Ser Gln Thr His Arg Val Asp  
180 185 190

Leu Gly Thr Leu Arg Gly Tyr Tyr Asn Gln Ser Glu Ala Gly Ser His  
195 200 205

Thr Val Gln Arg Met Tyr Gly Cys Asp Val Gly Ser Asp Trp Arg Phe  
210 215 220

Leu Arg Gly Tyr His Gln Tyr Ala Tyr Asp Gly Lys Asp Tyr Ile Ala  
225 230 235 240

Leu Lys Glu Asp Leu Arg Ser Trp Thr Ala Ala Asp Met Ala Ala Gln  
245 250 255

Thr Thr Lys His Lys Trp Glu Ala Ala His Val Ala Glu Gln Leu Arg  
260 265 270

Ala Tyr Leu Glu Gly Thr Cys Val Glu Trp Leu Arg Arg Tyr Leu Glu  
275 280 285

Asn Gly Lys Glu Thr Leu Gln Arg Thr Asp Ala Pro Lys Thr His Met  
290 295 300

Thr His His Ala Val Ser Asp His Glu Ala Thr Leu Arg Cys Trp Ala  
305 310 315 320

Leu Ser Phe Tyr Pro Ala Glu Ile Thr Leu Thr Trp Gln Arg Asp Gly  
325 330 335

Glu Asp Gln Thr Gln Asp Thr Glu Leu Val Glu Thr Arg Pro Ala Gly  
340 345 350

Asp Gly Thr Phe Gln Lys Trp Ala Ala Val Val Val Pro Ser Gly Gln  
355 360 365

Glu Gln Arg Tyr Thr Cys His Val Gln His Glu Gly Leu Pro Lys Pro  
370 375 380

Leu Thr Leu Arg Trp Glu Gln Ser Thr Arg Gly Gly Ala Ser Gly Gly  
385 390 395 400

Gly Leu Gly Gly Ile Phe Glu Ala Met Lys Met Glu Leu Arg Asp  
405 410 415

<210> 6  
<211> 280  
<212> PRT  
<213> Homo sapiens

&lt;400&gt; 6

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 Arg Gly Glu Pro Arg Phe Ile Ala Val Gly Tyr Val Asp Asp Thr Gln  
 20 25 30  
 Phe Val Arg Phe Asp Ser Asp Ala Ala Ser Gln Arg Met Glu Pro Arg  
 35 40 45  
 Ala Pro Trp Ile Glu Gln Glu Gly Pro Glu Tyr Trp Asp Gly Glu Thr  
 50 55 60  
 Arg Lys Val Lys Ala His Ser Gln Thr His Arg Val Asp Leu Gly Thr  
 65 70 75 80  
 Leu Arg Gly Tyr Tyr Asn Gln Ser Glu Ala Gly Ser His Thr Val Gln  
 85 90 95  
 Arg Met Tyr Gly Cys Asp Val Gly Ser Asp Trp Arg Phe Leu Arg Gly  
 100 105 110  
 Tyr His Gln Tyr Ala Tyr Asp Gly Lys Asp Tyr Ile Ala Leu Lys Glu  
 115 120 125  
 Asp Leu Arg Ser Trp Thr Ala Ala Asp Met Ala Ala Gln Thr Thr Lys  
 130 135 140  
 His Lys Trp Glu Ala Ala His Val Ala Glu Gln Leu Arg Ala Tyr Leu  
 145 150 155 160  
 Glu Gly Thr Cys Val Glu Trp Leu Arg Arg Tyr Leu Glu Asn Gly Lys  
 165 170 175  
 Glu Thr Leu Gln Arg Thr Asp Ala Pro Lys Thr His Met Thr His His  
 180 185 190  
 Ala Val Ser Asp His Glu Ala Thr Leu Arg Cys Trp Ala Leu Ser Phe  
 195 200 205  
 Tyr Pro Ala Glu Ile Thr Leu Thr Trp Gln Arg Asp Gly Glu Asp Gln  
 210 215 220  
 Thr Gln Asp Thr Glu Leu Val Glu Thr Arg Pro Ala Gly Asp Gly Thr  
 225 230 235 240  
 Phe Gln Lys Trp Ala Ala Val Val Val Pro Ser Gly Gln Glu Gln Arg  
 245 250 255  
 Tyr Thr Cys His Val Gln His Glu Gly Leu Pro Lys Pro Leu Thr Leu  
 260 265 270  
 Arg Trp Glu Gln Ser Thr Arg Gly  
 275 280

<210> 7  
 <211> 100  
 <212> PRT  
 <213> Homo sapiens

<400> 7

Met Ile Gln Arg Thr Pro Lys Ile Gln Val Tyr Ser Arg His Pro Ala  
 1 5 10 15

Glu Asn Gly Lys Ser Asn Phe Leu Asn Cys Tyr Val Ser Gly Phe His  
 20 25 30

Pro Ser Asp Ile Glu Val Asp Leu Leu Lys Asn Gly Glu Arg Ile Glu  
 35 40 45

Lys Val Glu His Ser Asp Leu Ser Phe Ser Lys Asp Trp Ser Phe Tyr  
 50 55 60

Leu Leu Tyr Tyr Thr Glu Phe Thr Pro Thr Glu Lys Asp Glu Tyr Ala  
 65 70 75 80

Cys Arg Val Asn His Val Thr Leu Ser Gln Pro Lys Ile Val Lys Trp  
 85 90 95

Asp Arg Asp Met  
 100

<210> 8  
 <211> 36  
 <212> DNA  
 <213> Artificial sequence

<220>  
 <223> Single strand DNA oligonucleotide

<400> 8  
 aggagatata catatgggct ctcactccat gaggta

36

<210> 9  
 <211> 43  
 <212> DNA  
 <213> Artificial sequence

<220>  
 <223> Single strand DNA oligonucleotide

<400> 9  
 cgggctttgt tagcaccgat tcataggtga ggggcttggg caa

43

<210> 10  
 <211> 15  
 <212> PRT  
 <213> Artificial sequence

<220>  
 <223> linker peptide

<400> 10

Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Ser  
 1 5 10 15

<210> 11  
 <211> 35  
 <212> DNA  
 <213> Artificial sequence  
  
 <220>  
 <223> Single strand DNA oligonucleotide  
  
 <400> 11  
 ggagatatac atatgatcca gcgtactcca aagat 35

<210> 12  
 <211> 49  
 <212> DNA  
 <213> Artificial sequence  
  
 <220>  
 <223> Single strand DNA oligonucleotide  
  
 <400> 12  
 cgggctttgt tagcagccga attcattaca tgtctcgatc ccacttaac 49

<210> 13  
 <211> 41  
 <212> DNA  
 <213> Artificial sequence  
  
 <220>  
 <223> Single strand DNA oligonucleotide  
  
 <400> 13  
 ggaagcggtt ggcgcatatg atccagcgta ctccaaagat t 41

<210> 14  
 <211> 50  
 <212> DNA  
 <213> Artificial sequence  
  
 <220>  
 <223> Single strand DNA oligonucleotide  
  
 <400> 14  
 ggaagcggcg gtggaggctc tggaggaggt ggcagcggct ctactccat 50

<210> 15  
 <211> 50  
 <212> DNA  
 <213> Artificial sequence  
  
 <220>  
 <223> Single strand DNA oligonucleotide  
  
 <400> 15  
 ggaagcggcg gtggaggctc tggaggaggt ggcagcggct ctactccat 50

<210> 16  
 <211> 43  
 <212> DNA  
 <213> Artificial sequence  
  
 <220>  
 <223> Single strand DNA oligonucleotide  
  
 <400> 16  
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<210> 17  
 <211> 14  
 <212> PRT  
 <213> Artificial sequence

<220>  
 <223> Specific biotinylation peptide sequence

<400> 17

Leu Gly Gly Ile Phe Glu Ala Met Lys Met Glu Leu Arg Asp  
 1 5 10

<210> 18  
 <211> 11  
 <212> PRT  
 <213> Artificial sequence

<220>  
 <223> Linker

<400> 18

Gln Ser Thr Arg Gly Gly Ala Ser Gly Gly Gly  
 1 5 10

<210> 19  
 <211> 100  
 <212> DNA  
 <213> Artificial sequence

<220>  
 <223> Single strand DNA oligonucleotide

<400> 19  
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 aaccacctcc ggaccgcga cctccctccc atctcagggt 100

<210> 20  
 <211> 39  
 <212> DNA  
 <213> Artificial sequence

<220>  
 <223> BirA recognition tag sequence

<400> 20  
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